In the Claims

Please amend the following claims according to the following listing of claims under 37 CFR 1.121.

Listing of Claims under 37 CFR 1.121:

What is claimed as new under Letters Patent of the United States:

1-90 (CANCELED)

91. (PREVIOUSLY ADDED): A composition for use in obtaining genotype data or sample allele frequency data, comprising: one or more copies of a set of oligonucleotides, the set of oligonucleotides being complementary to a group of two or more bi-allelic covering markers, wherein the set of oligonucleotides is selected for the set's utility to determine genotype data or sample allele frequency data for each of the two or more covering markers, wherein the group of covering markers is chosen so that a CL-F region is N covered to within [x, y] by the covering markers, wherein [x, y] is a two-dimensional distance, wherein x is less than or equal to 1 million base pairs and y is less than or equal to 0.2, N is an integer greater than or equal to 1, the covering markers and the CL-F region being for a species of creatures, the CL-F region being a collection of one or more points on a two-dimensional CL-F map that is similar to an x-y graph, the CL-F map having the two orthogonal dimensions of chromosomal location (CL) and least common allele frequency (F), whereby each point in the region is within the distance [x, y] of each of N or more of the covering markers,

wherein the CL-F region is a segment-subrange, whereby the segment-subrange is a rectangular region on the CL-F map, whereby the segment-subrange is bounded by a chromosomal segment and a least common allele frequency subrange, wherein the length of the segment of the segment-subrange is greater than or equal to the length of human chromosome 21, whereby the length of the segment is greater than or equal to about 47 million base pairs, wherein the subrange of the segment-subrange includes the least common allele frequency 0.1,

whereby there are at least about 24 covering markers with least common allele frequencies less than or equal to 0.3 that are distributed within the segment with a density of at least about 1 marker every two million base pairs.

92. (CURRENTLY AMENDED): A composition as in claim 91, ~~wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide or wherein each oligonucleotide in the set is a type (2) complementary oligonucleotide,~~ wherein the CL-F region is for the species of creatures and for a population, wherein the population is a population as in the field of population genetics and wherein each covering marker is an SNP.

93-104 (CANCELED)

105. (CURRENTLY AMENDED): A composition as in claim 92, wherein the subrange of the segment-subrange is the subrange 0 to 0.1, wherein N is greater than 2, whereby there are at least about 288 covering markers with least common allele frequencies less than or equal to 0.2 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs. ~~93, wherein the subrange of the segment-subrange is the subrange 0.1 to 0.2.~~

106-211 (CANCELED)

212. (CURRENTLY AMENDED): A composition as in claim 105,~~92, wherein each covering marker is an SNP,~~ wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific or wherein each oligonucleotide in the set has utility as a polymerase chain reaction primer, wherein the composition has utility to obtain genotype data or sample allele frequency data by generating a signal, wherein the signal is generated by the products of a polymerase chain reaction when oligonucleotides of the composition hybridize with one or more complementary alleles of one or more of the covering markers.

213-235 (CANCELED)

236. (NEW): A process of making a composition with utility for obtaining genotype data or sample allele frequency data, comprising:

choosing a group of covering markers so that a CL-F region is N covered to within [x, y] by the covering markers, wherein [x, y] is a two-dimensional distance, wherein x is less than or equal to 1 million base pairs and y is less than or equal to 0.2, N is an integer greater than or equal to 1, the covering markers and the CL-F region being for a species of creatures, the CL-F region being a collection of one or more points on a two-dimensional CL-F map that is similar to an x-y graph, the CL-F map having the two orthogonal dimensions of chromosomal location (CL) and least common allele frequency (F), whereby each point in the region is within the distance [x, y] of each of N or more of the covering markers, wherein the CL-F region is for the species of creatures and for a population, wherein the population is a population as in the field of population genetics,

wherein the CL-F region is a segment-subrange, whereby the segment-subrange is a rectangular region on the CL-F map, whereby the segment-subrange is bounded by a chromosomal segment and a least common allele frequency subrange, wherein the length of the segment of the segment-subrange is greater than or equal to the length of human chromosome 21, whereby the length of the segment is greater than or equal to about 47 million base pairs, wherein the subrange of the segment-subrange includes the least common allele frequency 0.1,
whereby there are at least about 24 covering markers with least common allele frequencies less than or equal to 0.3 that are distributed within the segment with a density of at least about 1 marker every two million base pairs;

selecting a set of oligonucleotides for the set's utility to determine genotype data or sample allele frequency data for each of the two or more covering markers, wherein the set of oligonucleotides is complementary to the group of two or more bi-allelic covering markers; and

including one or more copies of the set of oligonucleotides in the composition.

237. (NEW): A process as in claim 236, wherein each covering marker is an SNP.
238. (NEW): A process as in claim 237, wherein the subrange of the segment-subrange is the subrange 0 to 0.1, whereby there are at least about 24 covering markers with least common allele frequencies less than or equal to 0.2 that are distributed within the segment with a density of at least about 1 marker every two million base pairs.

239. (NEW): A process as in claim 238, wherein x is less than or equal to 250,000 base pairs, whereby there are at least about 96 covering markers with least common allele frequencies less than or equal to 0.2 that are distributed within the segment with a density of at least about 1 marker every five hundred thousand base pairs.

240. (NEW): A process as in claim 238, wherein y is 0.1, whereby there are at least about 24 covering markers with least common allele frequencies less than or equal to 0.1 that are distributed within the segment with a density of at least about 1 marker every two million base pairs.

241. (NEW): A process as in claim 239, wherein N is greater than 2, whereby there are at least about 288 covering markers with least common allele frequencies less than or equal to 0.2 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs.

242. (NEW): A process as in claim 240, wherein x is less than or equal to 250,000 base pairs, whereby there are at least about 96 covering markers with least common allele frequencies less than or equal to 0.1 that are distributed within the segment with a density of at least about 1 marker every five hundred thousand base pairs.

243. (NEW): A process as in claim 242, wherein N is greater than 2, whereby there are at least about 288 covering markers with least common allele frequencies less than or equal to 0.1 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs.

244. (NEW): A process as in claim 243, wherein the length of the segment of the segment-subrange is greater than or equal to the length of human chromosome number 6, whereby the length of the segment is greater than or equal to about 171 million base pairs, whereby there are at least about 1037 covering markers with least common allele frequencies less than or equal to 0.1 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs.

245. (NEW): A process as in claim 241, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.
246. (NEW): A process as in claim 243, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.
247. (NEW): A process as in claim 244, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.
248. (NEW): A process as in claim 238, wherein N is greater than 2, x is less than or equal to about 250,000 base pairs and y is less than or equal to about 0.1, whereby there are at least about 288 covering markers with least common allele frequencies less than or equal to about 0.1 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs.
249. (NEW): A process as in claim 248, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.
250. (NEW): A process as in claim 245, wherein the chosen group of covering markers includes thousands of bi-allelic markers.
251. (NEW): A process as in claim 246, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

252. (NEW): A process as in claim 249, wherein the chosen group of covering markers includes thousands of bi-allelic markers.

253. (NEW): A process as in claim 237, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

254. (NEW): A process as in claim 238, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

255. (NEW): A process as in claim 239, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

256. (NEW): A process as in claim 240, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

257. (NEW): A process as in claim 241, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

258. (NEW): A process as in claim 242, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

259. (NEW): A process as in claim 243, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

260. (NEW): A process as in claim 244, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

261. (NEW): A process as in claim 245, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

262. (NEW): A process as in claim 246, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

263. (NEW): A process as in claim 247, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

264. (NEW): A process as in claim 248, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

265. (NEW): A process as in claim 249, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

266. (NEW): A process as in claim 250, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

267. (NEW): A process as in claim 251, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

268. (NEW): A process as in claim 252, wherein the process comprises: including the composition in a sensor, wherein the sensor has utility to sense the presence of each allele of each marker in the group of covering markers by the generation of a physico-chemical signal, wherein the generation of the signal occurs due to one or more oligonucleotides that are complementary to a particular allele hybridizing with chromosomal DNA specimens of the particular allele, wherein the composition includes the one or more oligonucleotides that are complementary to the particular allele.

269. (NEW): A process as in claim 237, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific.
270. (NEW): A process as in claim 241, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific.
271. (NEW): A process as in claim 243, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific.
272. (NEW): A process as in claim 245, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific.
273. (NEW): A process as in claim 246, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific.
274. (NEW): A process as in claim 247, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific.
275. (NEW): A process as in claim 248, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific.
276. (NEW): A process as in claim 249, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific.
277. (NEW): A process as in claim 250, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific.
278. (NEW): A process as in claim 251, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific.

279. (NEW): A process as in claim 252, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific.

280. (NEW): A process as in claim 269, wherein the process comprises: including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide or a silicon chip, wherein the composition comprises copies of the set of oligonucleotides.

281. (NEW): A process as in claim 270, wherein the process comprises: including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide or a silicon chip, wherein the composition comprises copies of the set of oligonucleotides.

282. (NEW): A process as in claim 271, wherein the process comprises: including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide or a silicon chip, wherein the composition comprises copies of the set of oligonucleotides.

283. (NEW): A process as in claim 272, wherein the process comprises: including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide or a silicon chip, wherein the composition comprises copies of the set of oligonucleotides.

284. (NEW): A process as in claim 273, wherein the process comprises: including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide or a silicon chip, wherein the composition comprises copies of the set of oligonucleotides.

285. (NEW): A process as in claim 274, wherein the process comprises: including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide or a silicon chip, wherein the composition comprises copies of the set of oligonucleotides.

286. (NEW): A process as in claim 275, wherein the process comprises: including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide or a silicon chip, wherein the composition comprises copies of the set of oligonucleotides.

287. (NEW): A process as in claim 276, wherein the process comprises: including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide or a silicon chip, wherein the composition comprises copies of the set of oligonucleotides.

288. (NEW): A process as in claim 277, wherein the process comprises: including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide, wherein the composition comprises copies of the set of oligonucleotides.

289. (NEW): A process as in claim 278, wherein the process comprises: including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide, wherein the composition comprises copies of the set of oligonucleotides.

290. (NEW): A process as in claim 279, wherein the process comprises: including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide, wherein the composition comprises copies of the set of oligonucleotides.

291. (NEW): A process as in claim 237, wherein each oligonucleotide in the set has utility as a polymerase chain reaction primer, wherein the composition has utility to obtain genotype data or sample allele frequency data by generating a signal, wherein the signal is generated by the products of a polymerase chain reaction due to oligonucleotides of the composition hybridizing with one or more complementary alleles of one or more of the covering markers.

292. (NEW): A process as in claim 241, wherein each oligonucleotide in the set has utility as a polymerase chain reaction primer, wherein the composition has utility to obtain genotype data or sample allele frequency data by generating a signal, wherein the signal is generated by the products of a polymerase chain reaction due to oligonucleotides of the composition hybridizing with one or more complementary alleles of one or more of the covering markers.

293. (NEW): A process as in claim 243, wherein each oligonucleotide in the set has utility as a polymerase chain reaction primer, wherein the composition has utility to obtain genotype data or sample allele frequency data by generating a signal, wherein the signal is generated by the products of a polymerase chain reaction due to oligonucleotides of the composition hybridizing with one or more complementary alleles of one or more of the covering markers.

294. (NEW): A process as in claim 246, wherein each oligonucleotide in the set has utility as a polymerase chain reaction primer, wherein the composition has utility to obtain genotype data or sample allele frequency data by generating a signal, wherein the signal is generated by the products of a polymerase chain reaction due to oligonucleotides of the composition hybridizing with one or more complementary alleles of one or more of the covering markers.

295. (NEW): A process as in claim 248, wherein each oligonucleotide in the set has utility as a polymerase chain reaction primer, wherein the composition has utility to obtain genotype data or sample allele frequency data by generating a signal, wherein the signal is generated by the products of a polymerase chain reaction due to oligonucleotides of the composition hybridizing with one or more complementary alleles of one or more of the covering markers.

296. (NEW): A process as in claim 249, wherein each oligonucleotide in the set has utility as a polymerase chain reaction primer, wherein the composition has utility to obtain genotype data or sample allele frequency data by generating a signal, wherein the signal is generated by the products of a polymerase chain reaction due to oligonucleotides of the composition hybridizing with one or more complementary alleles of one or more of the covering markers.

297. (NEW): A process as in claim 250, wherein each oligonucleotide in the set has utility as a polymerase chain reaction primer, wherein the composition has utility to obtain genotype data or sample allele frequency data by generating a signal, wherein the signal is generated by the products of a polymerase chain reaction due to oligonucleotides of the composition hybridizing with one or more complementary alleles of one or more of the covering markers.
298. (NEW): A process as in claim 251, wherein each oligonucleotide in the set has utility as a polymerase chain reaction primer, wherein the composition has utility to obtain genotype data or sample allele frequency data by generating a signal, wherein the signal is generated by the products of a polymerase chain reaction due to oligonucleotides of the composition hybridizing with one or more complementary alleles of one or more of the covering markers.

299. (NEW): A process as in claim 252, wherein each oligonucleotide in the set has utility as a polymerase chain reaction primer, wherein the composition has utility to obtain genotype data or sample allele frequency data by generating a signal, wherein the signal is generated by the products of a polymerase chain reaction due to oligonucleotides of the composition hybridizing with one or more complementary alleles of one or more of the covering markers.

300. (NEW): A process of using a composition as in claim 92 to obtain genotype data or sample allele frequency data.
301. (NEW): A process of using a composition as in claim 105 to obtain genotype data or sample allele frequency data.
302. (NEW): A process of using a composition as in claim 212 to obtain genotype data or sample allele frequency data.

303. (NEW): A process of making a composition with utility for obtaining genotype data or sample allele frequency data, comprising:

choosing a group of covering markers so that a CL-F region is N covered to within [x, y] by the covering markers, wherein [x, y] is a two-dimensional distance, wherein x is less than or equal to 1 million base pairs and y is less than or equal to 0.2, N is an integer greater than or equal to 1, the covering markers and the CL-F region being for a species of creatures, the CL-F region being a collection of one or more points on a two-dimensional CL-F map that is similar to an x-y graph, the CL-F map having the two orthogonal dimensions of chromosomal location (CL) and least common allele frequency (F), whereby each point in the region is within the distance [x, y] of each of N or more of the covering markers, wherein the CL-F region is for the species of creatures and for a population, wherein the population is a population as in the field of population genetics, wherein each covering marker is an SNP,

wherein the CL-F region is a segment-subrange, whereby the segment-subrange is a rectangular region on the CL-F map, whereby the segment-subrange is bounded by a chromosomal segment and a least common allele frequency subrange, wherein the length of the segment of the segment-subrange is greater than or equal to the length of human chromosome 21, whereby the length of the segment is greater than or equal to about 47 million base pairs, wherein the subrange of the segment-subrange includes the least common allele frequency 0.1,

whereby there are at least about 24 covering markers with least common allele frequencies less than or equal to 0.3 that are distributed within the segment with a density of at least about 1 marker every two million base pairs;

selecting a set of oligonucleotides for the set's utility to determine genotype data or sample allele frequency data for each of the two or more covering markers, wherein there is an oligonucleotide in the set that is complementary to each of one or more alleles of each marker in the group of two or more bi-allelic covering markers; and

including one or more copies of the set of oligonucleotides in the composition.

304. (NEW): A process as in claim 303, wherein there is an oligonucleotide in the set that is allele-specific and is type (1) complementary to one of the two alleles of each bi-allelic covering marker in the group of covering markers, wherein each bi-allelic covering marker in the group of covering markers is an exact bi-allelic marker.

305. (NEW): A process as in claim 304, wherein the process comprises: including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide or a silicon chip, wherein the composition comprises copies of the set of oligonucleotides.

306. (NEW): A process as in claim 304, wherein the subrange of the segment-subrange is the subrange 0 to 0.1, wherein y is less than or equal to about 0.1, wherein x is less than or equal to about 250,000 base pairs, wherein N is greater than 2, whereby there are at least about 288 covering markers with least common allele frequencies less than or equal to about 0.1 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs, wherein the species is human and the chromosomal location coordinates of CL-F points in the CL-F region range over an entire human chromosome, whereby the length of the segment of the segment-subrange is the length of the entire human chromosome over which the chromosomal location coordinates of CL-F points in the CL-F region range.

307. (NEW): A process as in claim 306, wherein the process comprises:

including the composition in an array by attaching the oligonucleotides comprised in the composition to a glass slide, wherein the chosen group of covering markers includes thousands of bi-allelic markers.